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## SEQUENCE LISTING

#6

TECH CENTER 1600/2900

JAN 14 2002

RECEIVED

<10> DING, SHI-YOU  
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<120> THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS  
CELLULOLYTICUS

<130> 40170.6US01

<140> 09/917,383  
<141> 2001-07-28

<160> 14

<170> PatentIn Ver. 2.1

<210> 1  
<211> 1228  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Segment of  
GuxA

<400> 1  
Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly  
1 5 10 15  
Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu  
20 25 30  
Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln  
35 40 45  
His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala  
50 55 60  
Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala  
65 70 75 80  
Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser  
85 90 95  
Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly  
100 105 110  
Val Asn Gly Gly Pro Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser  
115 120 125  
Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp  
130 135 140

Leu	Pro	Gly	Arg	Asp	Cys	Ala	Ala	Leu	Ala	Ser	Asn	Gly	Glu	Leu	Pro	145	150	155	160
Ala	Thr	Ala	Ala	Gly	Leu	Gln	Thr	Tyr	Glu	Thr	Gln	Tyr	Ile	Asp	Pro	165	170		175
Ile	Ala	Ser	Ile	Leu	Ser	Asn	Pro	Lys	Tyr	Ser	Ser	Leu	Arg	Ile	Val	180	185		190
Thr	Ile	Ile	Glu	Pro	Asp	Ser	Leu	Pro	Asn	Ala	Val	Thr	Asn	Met	Ser	195	200	205	
Ile	Gln	Ala	Cys	Ala	Thr	Ala	Val	Pro	Tyr	Tyr	Glu	Gln	Gly	Ile	Glu	210	215	220	
Tyr	Ala	Leu	Thr	Lys	Leu	His	Ala	Ile	Pro	Asn	Val	Tyr	Ile	Tyr	Met	225	230	235	240
Asp	Ala	Ala	His	Ser	Gly	Trp	Leu	Gly	Trp	Pro	Asn	Asn	Ala	Ser	Gly	245	250		255
Tyr	Val	Gln	Glu	Val	Gln	Lys	Val	Leu	Asn	Ala	Ser	Ile	Gly	Val	Asn	260	265		270
Gly	Ile	Asp	Gly	Phe	Val	Thr	Asn	Thr	Ala	Asn	Tyr	Thr	Pro	Leu	Lys	275	280		285
Glu	Pro	Phe	Met	Thr	Ala	Thr	Gln	Gln	Val	Gly	Gly	Gln	Pro	Val	Glu	290	295	300	
Ser	Ala	Asn	Phe	Tyr	Gln	Trp	Asn	Pro	Asp	Ile	Asp	Glu	Ala	Asp	Tyr	305	310	315	320
Ala	Val	Asp	Leu	Tyr	Ser	Arg	Leu	Val	Ala	Ala	Gly	Phe	Pro	Ser	Ser	325	330		335
Ile	Gly	Met	Leu	Ile	Asp	Thr	Leu	Arg	Asn	Gly	Trp	Gly	Gly	Pro	Asn	340	345		350
Glu	Pro	Thr	Gly	Pro	Ser	Thr	Ala	Thr	Asp	Val	Asn	Thr	Phe	Val	Asn	355	360		365
Gln	Ser	Lys	Ile	Asp	Leu	Arg	Gln	His	Arg	Gly	Leu	Trp	Cys	Asn	Gln	370	375	380	
Asn	Gly	Ala	Gly	Leu	Gly	Gln	Pro	Pro	Gln	Ala	Ser	Pro	Thr	Asp	Phe	385	390	395	400
Pro	Asn	Ala	His	Leu	Asp	Ala	Tyr	Val	Trp	Ile	Lys	Pro	Pro	Gly	Glu	405	410		415
Ser	Asp	Gly	Thr	Ser	Ala	Ala	Ser	Asp	Pro	Thr	Thr	Gly	Lys	Lys	Ser	420	425		430
Asp	Pro	Met	Cys	Asp	Pro	Thr	Tyr	Thr	Thr	Ser	Tyr	Gly	Val	Leu	Thr	435	440	445	

Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln  
 450 455 460  
 Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Pro Thr Ser Thr  
 465 470 475 480  
 Ser Ser Ser Pro Pro Pro Pro Pro Pro Ser Pro Ser Ala Ser Pro Ser  
 485 490 495  
 Pro Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser  
 500 505 510  
 Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser  
 515 520 525  
 Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser  
 530 535 540  
 Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser  
 545 550 555 560  
 Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Ser Ser Ser Pro Ser  
 565 570 575  
 Pro Ser Pro Thr Ser Ser Pro Val Ser Gly Gly Leu Lys Val Gln Tyr  
 580 585 590  
 Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln Ile Lys Pro Gly Leu  
 595 600 605  
 Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr  
 610 615 620  
 Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr  
 625 630 635 640  
 Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn Ile Arg Ala Ser Phe  
 645 650 655  
 Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Leu  
 660 665 670  
 Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly Ser Thr Gly Glu Ile  
 675 680 685  
 Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn Phe Thr Glu Thr Asn  
 690 695 700  
 Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln Asp Trp Thr Lys Val  
 705 710 715 720  
 Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly Thr Glu Pro Ser Gly  
 725 730 735  
 Thr Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser  
 740 745 750

Pro Gly Gly Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val	755	760	765
Thr Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr	770	775	780
Asp Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu	785	790	795
Val Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala	805	810	815
Gly Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn	820	825	830
Thr Ser Ala Pro Ser Thr Pro Val Thr Ala Thr Thr Thr Ser Pro Ser	835	840	845
Pro Ser Pro Thr Pro Thr Gly Thr Thr Val Thr Asp Cys Thr Pro Gly	850	855	860
Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp Glu Tyr Arg Val	865	870	875
Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn	885	890	895
Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly	900	905	910
Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His	915	920	925
Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser	930	935	940
Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser	945	950	955
Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr	965	970	975
Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser	980	985	990
Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr	995	1000	1005
Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp	1010	1015	1020
Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn	1025	1030	1035
Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala Arg Gly Ser Leu	1045	1050	1055

Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp  
 1060 1065 1070  
 Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr  
 1075 1080 1085  
 Ser Gly Thr Ser Ser Pro Thr Pro Ser Pro Ser Pro Thr Pro Thr Pro  
 1090 1095 1100  
 Ser Pro Thr Pro Thr Pro Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro  
 1105 1110 1115 1120  
 Thr Ser Ser Pro Ser Ser Ser Gly Val Ala Cys Arg Ala Thr Tyr Val  
 1125 1130 1135  
 Val Asn Ser Asp Trp Gly Ser Gly Phe Thr Ala Thr Val Thr Val Thr  
 1140 1145 1150  
 Asn Thr Gly Ser Arg Ala Thr Asn Gly Trp Thr Val Ala Trp Ser Phe  
 1155 1160 1165  
 Gly Gly Asn Gln Thr Val Thr Asn Tyr Trp Asn Thr Ala Leu Thr Gln  
 1170 1175 1180  
 Ser Gly Ala Ser Val Thr Ala Thr Asn Leu Ser Tyr Asn Asn Val Ile  
 1185 1190 1195 1200  
 Gln Pro Gly Gln Ser Thr Thr Phe Gly Phe Asn Gly Ser Tyr Ser Gly  
 1205 1210 1215  
 Thr Asn Ala Ala Pro Thr Leu Ser Cys Thr Ala Ser  
 1220 1225

<210> 2

<211> 3687

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
GuxA

<400> 2

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cccgccatct	caaaacggct	gcgagccggc	gtcctcgccg	gggcggtgag	catcgagcc	120
tccatcgtag	cgctggcgat	gcagcatcct	gccatcgccg	cgacgcacgt	cgacaatccc	180
tatgcgggag	cgaccttctt	cgtcaaccgc	tactgggccc	aagaagtaca	gagcgaagcg	240
gcgaaccaga	ccaatgccac	tctcgagcgc	aaaatgcgcg	tcgtttccac	atattcgacg	300
gccgtctgga	tggaccgcat	cgctgcgacg	aacggcgctc	acggcggacc	cggcttgacg	360
acatatctgg	acgccgccct	ctcccagcag	cagggaaacca	cccctgaagt	cattgagatt	420
gtcatctacg	atctgccggg	acgcgactgc	gcggcgctcg	cctccaacgg	cgaactgccc	480
gctacggcag	caggtttgca	gacctatgaa	acgcagtaca	tcgatccgat	tgcgagtatc	540
ctgagcaatc	cgaagtactc	cagcctgcgg	atcgtgacga	tcattgagcc	ggactcgctg	600
ccaaacgcgg	tcaccaatat	gagcattcaa	gcgtgtgcaa	cggcggtgcc	gtattacgag	660
caaggcatcg	agtaacgcgt	cacgaaattg	cacgccattc	cgaacgtgta	catctacatg	720
gacgcgcccc	actccggctg	gcttgggtgg	cccaataatg	ccagcggata	cgtacaggaa	780
gtccagaagg	tcctcaacgc	gagcatcggg	gtcaacggca	tcgacggctt	cgtcaccaac	840

acggcggaatt	acacgccgtt	gaaggagccg	ttcatgaccg	ccaccagca	ggtcggcgga	900
cagccggtgg	agtcggcgaa	tttctaccag	tggaaatcctg	acatcgacga	agccgactac	960
gcggttgact	tgtactcgcg	gctcgtcgcc	gctggctttc	caagcagcat	cggcatgctc	1020
atcgacacct	tacgcaacgg	ttgggggtgg	ccgaacgaac	caacaggccc	gagcaccgcg	1080
accgatgtca	acaccttcgt	caaccagtcg	aagattgacc	ttcggcagca	ccgcggcctg	1140
tgggtgcaacc	agaacgggtgc	gggcctcggc	cagccgccgc	aggcaagccc	gacggacttc	1200
ccgaacgcgc	acctcgacgc	gtatgtctgg	atcaagccgc	cgggtgagtc	ggacggcaca	1260
agcgctgcga	gcgatccgac	aactggcaag	aagtcggacc	ccatgtgcga	cccgcgtac	1320
acgacgtcgt	acgggggtact	gaccaacgcg	ttaccgaact	ccccgatcgc	cggccagtgg	1380
ttcccggcgc	agtttgacca	gcttgctcgc	aacgcacggc	cagcgggtgcc	gacgtcgacc	1440
agctcgagcc	cgccgcctcc	gccgccgagt	ccgtcggctt	cgccgagtc	gagccccagt	1500
ccgagcccga	gcagctcgcc	atcgccgtcg	ccgtctccga	gctcgagccc	gtctccgtcg	1560
ccgagcccga	gtccgagccc	gagtagctcg	ccgtcgccgt	ctccgagctc	gagcccgatc	1620
ccgtcgccga	gcccagatcc	gagcccgagt	agctcgccgt	cgccgtctcc	gagctcgagc	1680
ccgtctccgt	cgccgagccc	gagtccgagc	ccgagtagct	cgccgtcgcc	gtctccgacg	1740
tcgtcgccgg	tgtcgggtgg	gctgaagggtg	cagtacaaga	acaatgattc	ggcgccgggt	1800
gataaccaga	tcaaaccggg	tctccagttg	gtgaataaccg	ggtcgtcgtc	ggtggatttg	1860
tcgacgggtga	cggtgcggta	ctggttcacc	cgggatgggtg	ggtcgtcgac	actggtgtac	1920
aactgtgact	gggcggcgat	gggggtgtggg	aatatccgcg	cctcgttcgg	ctcgggtgaac	1980
ccggcgacgc	cgacggcgga	cacctacctg	cagttgtcgt	tcactggtgg	aacggtggcc	2040
gctgggtggg	cgacgggtga	gattcaaaac	cgggtgaata	agagtgactg	gtcgaatttc	2100
accgagacca	atgactactc	gtatgggacg	aacaccacct	tccaggactg	gacgaagggtg	2160
acggtgtacg	tcaacggcgt	gttgggtgtgg	gggactgaac	cgcccgccac	cagccccagc	2220
cccacaccat	ccccgagccc	gagcccgagc	ccgagcccgg	gtggggatgt	gacgccgccg	2280
agtgtgccga	ccggcttggg	ggtgacgggg	gtgagtggtg	cgccggtgtc	gttggcggtg	2340
aatgcgtcga	cggataacgt	gggggtggcg	cattacaacg	tgtaccgcaa	cgggggtgtg	2400
gtggggccagc	cgacgggtgac	ctcgttcacc	gacacggggt	tggccgcggg	aaccgcgtac	2460
acctacacgg	tggccgcggg	ggacgctgcg	ggtaaacacct	ccgccccatc	cacccccgtc	2520
accgccacca	ccacgagtcc	cagccccagc	cccacgcgca	cggggaccac	ggtcaccgac	2580
tgcacgcccc	gtcctaacca	gaatgggtgtg	accagcgtgc	agggcgacga	ataccgggtg	2640
cagaccaatg	agtggaaattc	gtcggcccag	cagtgccctca	ccatcaatac	cgcgaccggt	2700
gcctggacgg	tgagcactgc	gaacttcagc	ggtgggaccg	gcggtgcgcc	cgcgacgtat	2760
ccgtcgatct	acaagggctg	ccactggggc	aactgcacca	cgaagaacgt	cgggatgccg	2820
attcagatca	gtcagattgg	ttcggctgtg	acgtcgtgga	gtacgacgca	ggtgtcgctc	2880
ggcgcgatatg	acgtggccta	cgacattttg	acgaacagta	ccccaacgac	aaccggtcag	2940
ccaaacggta	ccgaaatcat	gatttggctg	aattcgcggtg	gtgggggtgca	gccgttcggg	3000
tcgcagacag	cgacgggtgt	gacggtcgct	ggtcacacgt	ggaatgtctg	gcagggtcag	3060
cagacctcgt	ggaagattat	ttcctacgtc	ctgacccccg	gtgcgacgtc	gatcagtaat	3120
ctggatttga	agggcatttt	cgcgacgcc	cgggcacgcg	ggtcgctcaa	cacctccgat	3180
tacctgctcg	acgttgaggc	cgggtttgag	atctggcaag	gtggtcaggg	cctggggcagc	3240
aactcgttca	gcgtctccgt	gacgagcggc	acgtccagcc	cgacaccgag	cccagagccc	3300
acgccgacac	cgagcccgcg	gccgacaccg	tctccgagcc	cgacccccgtc	gccgagtcgg	3360
accagctcgc	cgtcgtcgtc	gggtgtggcg	tgccgggcga	cgtatgtggt	gaatagtgat	3420
tggggttctg	ggtttacggc	gacgggtgacg	gtgacgaata	ccgggagccg	ggcgacgaac	3480
gggtggacgg	tggcgtggtc	gtttggtggg	aatcagacgg	tcacgaacta	ctggaacact	3540
gcgttgaccc	aatcaggtgc	atcgggtgacg	gcgacgaacc	tgagttacaa	caacgtgatc	3600
caaccgggtc	agtcgaccac	cttcggattc	aacggaagtt	actcaggaac	aaacgccgcg	3660
ccgacgctca	gctgcacagc	cagctga				3687

&lt;210&gt; 3

&lt;211&gt; 53

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Segment of  
GuxA

&lt;400&gt; 3

Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly  
 1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu  
 20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln  
 35 40 45

His Pro Ala Ile Ala  
 50

&lt;210&gt; 4

&lt;211&gt; 423

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Segment of  
 GuxA

&lt;400&gt; 4

Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn  
 1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn  
 20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala  
 35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro  
 50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr  
 65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp  
 85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly  
 100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu  
 115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro  
 130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala  
 145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys  
 165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser  
 180 185 190  
 Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val  
 195 200 205  
 Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe  
 210 215 220  
 Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr  
 225 230 235 240  
 Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr  
 245 250 255  
 Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr  
 260 265 270  
 Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile  
 275 280 285  
 Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro  
 290 295 300  
 Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp  
 305 310 315 320  
 Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu  
 325 330 335  
 Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu  
 340 345 350  
 Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser  
 355 360 365  
 Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp  
 370 375 380  
 Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn  
 385 390 395 400  
 Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val  
 405 410 415  
 Ala Asn Ala Arg Pro Ala Val  
 420

<210> 5

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
GuxA



&lt;400&gt; 5

Val	Ser	Gly	Gly	Leu	Lys	Val	Gln	Tyr	Lys	Asn	Asn	Asp	Ser	Ala	Pro
1				5					10					15	

Gly	Asp	Asn	Gln	Ile	Lys	Pro	Gly	Leu	Gln	Leu	Val	Asn	Thr	Gly	Ser
			20					25					30		

Ser	Ser	Val	Asp	Leu	Ser	Thr	Val	Thr	Val	Arg	Tyr	Trp	Phe	Thr	Arg
		35					40					45			

Asp	Gly	Gly	Ser	Ser	Thr	Leu	Val	Tyr	Asn	Cys	Asp	Trp	Ala	Ala	Met
	50					55					60				

Gly	Cys	Gly	Asn	Ile	Arg	Ala	Ser	Phe	Gly	Ser	Val	Asn	Pro	Ala	Thr
65					70					75					80

Pro	Thr	Ala	Asp	Thr	Tyr	Leu	Gln	Leu	Ser	Phe	Thr	Gly	Gly	Thr	Leu
				85					90					95	

Ala	Ala	Gly	Gly	Ser	Thr	Gly	Glu	Ile	Gln	Asn	Arg	Val	Asn	Lys	Ser
			100					105					110		

Asp	Trp	Ser	Asn	Phe	Thr	Glu	Thr	Asn	Asp	Tyr	Ser	Tyr	Gly	Thr	Asn
		115					120					125			

Thr	Thr	Phe	Gln	Asp	Trp	Thr	Lys	Val	Thr	Val	Tyr	Val	Asn	Gly	Val
	130					135					140				

Leu	Val	Trp	Gly	Thr	Glu
145					150

&lt;210&gt; 6

&lt;211&gt; 1043

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Segment of GuxA

&lt;400&gt; 6

Met	Glu	Arg	Thr	Gln	Gln	Ser	Gly	Arg	Asn	Cys	Arg	Tyr	Gln	Arg	Gly
1				5					10					15	

Thr	Thr	Arg	Met	Pro	Ala	Ile	Ser	Lys	Arg	Leu	Arg	Ala	Gly	Val	Leu
			20					25					30		

Ala	Gly	Ala	Val	Ser	Ile	Ala	Ala	Ser	Ile	Val	Pro	Leu	Ala	Met	Gln
		35					40					45			

His	Pro	Ala	Ile	Ala	Ala	Thr	His	Val	Asp	Asn	Pro	Tyr	Ala	Gly	Ala
	50					55					60				

Thr	Phe	Phe	Val	Asn	Pro	Tyr	Trp	Ala	Gln	Glu	Val	Gln	Ser	Glu	Ala
	65				70					75				80	

Ala	Asn	Gln	Thr	Asn	Ala	Thr	Leu	Ala	Ala	Lys	Met	Arg	Val	Val	Ser	85	90	95
Thr	Tyr	Ser	Thr	Ala	Val	Trp	Met	Asp	Arg	Ile	Ala	Ala	Ile	Asn	Gly	100	105	110
Val	Asn	Gly	Gly	Pro	Gly	Leu	Thr	Thr	Tyr	Leu	Asp	Ala	Ala	Leu	Ser	115	120	125
Gln	Gln	Gln	Gly	Thr	Thr	Pro	Glu	Val	Ile	Glu	Ile	Val	Ile	Tyr	Asp	130	135	140
Leu	Pro	Gly	Arg	Asp	Cys	Ala	Ala	Leu	Ala	Ser	Asn	Gly	Glu	Leu	Pro	145	150	155
Ala	Thr	Ala	Ala	Gly	Leu	Gln	Thr	Tyr	Glu	Thr	Gln	Tyr	Ile	Asp	Pro	165	170	175
Ile	Ala	Ser	Ile	Leu	Ser	Asn	Pro	Lys	Tyr	Ser	Ser	Leu	Arg	Ile	Val	180	185	190
Thr	Ile	Ile	Glu	Pro	Asp	Ser	Leu	Pro	Asn	Ala	Val	Thr	Asn	Met	Ser	195	200	205
Ile	Gln	Ala	Cys	Ala	Thr	Ala	Val	Pro	Tyr	Tyr	Glu	Gln	Gly	Ile	Glu	210	215	220
Tyr	Ala	Leu	Thr	Lys	Leu	His	Ala	Ile	Pro	Asn	Val	Tyr	Ile	Tyr	Met	225	230	235
Asp	Ala	Ala	His	Ser	Gly	Trp	Leu	Gly	Trp	Pro	Asn	Asn	Ala	Ser	Gly	245	250	255
Tyr	Val	Gln	Glu	Val	Gln	Lys	Val	Leu	Asn	Ala	Ser	Ile	Gly	Val	Asn	260	265	270
Gly	Ile	Asp	Gly	Phe	Val	Thr	Asn	Thr	Ala	Asn	Tyr	Thr	Pro	Leu	Lys	275	280	285
Glu	Pro	Phe	Met	Thr	Ala	Thr	Gln	Gln	Val	Gly	Gly	Gln	Pro	Val	Glu	290	295	300
Ser	Ala	Asn	Phe	Tyr	Gln	Trp	Asn	Pro	Asp	Ile	Asp	Glu	Ala	Asp	Tyr	305	310	315
Ala	Val	Asp	Leu	Tyr	Ser	Arg	Leu	Val	Ala	Ala	Gly	Phe	Pro	Ser	Ser	325	330	335
Ile	Gly	Met	Leu	Ile	Asp	Thr	Leu	Arg	Asn	Gly	Trp	Gly	Gly	Pro	Asn	340	345	350
Glu	Pro	Thr	Gly	Pro	Ser	Thr	Ala	Thr	Asp	Val	Asn	Thr	Phe	Val	Asn	355	360	365
Gln	Ser	Lys	Ile	Asp	Leu	Arg	Gln	His	Arg	Gly	Leu	Trp	Cys	Asn	Gln	370	375	380

Asn	Gly	Ala	Gly	Leu	Gly	Gln	Pro	Pro	Gln	Ala	Ser	Pro	Thr	Asp	Phe	385	390	395	400
Pro	Asn	Ala	His	Leu	Asp	Ala	Tyr	Val	Trp	Ile	Lys	Pro	Pro	Gly	Glu	405	410		415
Ser	Asp	Gly	Thr	Ser	Ala	Ala	Ser	Asp	Pro	Thr	Thr	Gly	Lys	Lys	Ser	420	425	430	
Asp	Pro	Met	Cys	Asp	Pro	Thr	Tyr	Thr	Thr	Ser	Tyr	Gly	Val	Leu	Thr	435	440	445	
Asn	Ala	Leu	Pro	Asn	Ser	Pro	Ile	Ala	Gly	Gln	Trp	Phe	Pro	Ala	Gln	450	455	460	
Phe	Asp	Gln	Leu	Val	Ala	Asn	Ala	Arg	Pro	Ala	Val	Val	Ser	Gly	Gly	465	470	475	480
Leu	Lys	Val	Gln	Tyr	Lys	Asn	Asn	Asp	Ser	Ala	Pro	Gly	Asp	Asn	Gln	485	490	495	
Ile	Lys	Pro	Gly	Leu	Gln	Leu	Val	Asn	Thr	Gly	Ser	Ser	Ser	Val	Asp	500	505	510	
Leu	Ser	Thr	Val	Thr	Val	Arg	Tyr	Trp	Phe	Thr	Arg	Asp	Gly	Gly	Ser	515	520	525	
Ser	Thr	Leu	Val	Tyr	Asn	Cys	Asp	Trp	Ala	Ala	Met	Gly	Cys	Gly	Asn	530	535	540	
Ile	Arg	Ala	Ser	Phe	Gly	Ser	Val	Asn	Pro	Ala	Thr	Pro	Thr	Ala	Asp	545	550	555	560
Thr	Tyr	Leu	Gln	Leu	Ser	Phe	Thr	Gly	Gly	Thr	Leu	Ala	Ala	Gly	Gly	565	570	575	
Ser	Thr	Gly	Glu	Ile	Gln	Asn	Arg	Val	Asn	Lys	Ser	Asp	Trp	Ser	Asn	580	585	590	
Phe	Thr	Glu	Thr	Asn	Asp	Tyr	Ser	Tyr	Gly	Thr	Asn	Thr	Thr	Phe	Gln	595	600	605	
Asp	Trp	Thr	Lys	Val	Thr	Val	Tyr	Val	Asn	Gly	Val	Leu	Val	Trp	Gly	610	615	620	
Thr	Glu	Asp	Val	Thr	Pro	Pro	Ser	Val	Pro	Thr	Gly	Leu	Val	Val	Thr	625	630	635	640
Gly	Val	Ser	Gly	Ser	Ser	Val	Ser	Leu	Ala	Trp	Asn	Ala	Ser	Thr	Asp	645	650	655	
Asn	Val	Gly	Val	Ala	His	Tyr	Asn	Val	Tyr	Arg	Asn	Gly	Val	Leu	Val	660	665	670	
Gly	Gln	Pro	Thr	Val	Thr	Ser	Phe	Thr	Asp	Thr	Gly	Leu	Ala	Ala	Gly	675	680	685	

Thr	Ala	Tyr	Thr	Tyr	Thr	Val	Ala	Ala	Val	Asp	Ala	Ala	Gly	Asn	Thr	690	695	700
Ser	Ala	Pro	Ser	Thr	Pro	Val	Asp	Cys	Thr	Pro	Gly	Pro	Asn	Gln	Asn	705	710	715
Gly	Val	Thr	Ser	Val	Gln	Asp	Gly	Glu	Tyr	Arg	Val	Gln	Thr	Asn	Glu	725	730	735
Trp	Asn	Ser	Ser	Ala	Gln	Gln	Cys	Leu	Thr	Ile	Asn	Thr	Ala	Thr	Gly	740	745	750
Ala	Trp	Thr	Val	Ser	Thr	Ala	Asn	Phe	Ser	Gly	Gly	Thr	Gly	Gly	Ala	755	760	765
Pro	Ala	Thr	Tyr	Pro	Ser	Ile	Tyr	Lys	Gly	Cys	His	Trp	Gly	Asn	Cys	770	775	780
Thr	Thr	Lys	Asn	Val	Gly	Met	Pro	Ile	Gln	Ile	Ser	Gln	Ile	Gly	Ser	785	790	795
Ala	Val	Thr	Ser	Trp	Ser	Thr	Thr	Gln	Val	Ser	Ser	Gly	Ala	Tyr	Asp	805	810	815
Val	Ala	Tyr	Asp	Ile	Trp	Thr	Asn	Ser	Thr	Pro	Thr	Thr	Thr	Gly	Gln	820	825	830
Pro	Asn	Gly	Thr	Glu	Ile	Met	Ile	Trp	Leu	Asn	Ser	Arg	Gly	Gly	Val	835	840	845
Gln	Pro	Phe	Gly	Ser	Gln	Thr	Ala	Thr	Gly	Val	Thr	Val	Ala	Gly	His	850	855	860
Thr	Trp	Asn	Val	Trp	Gln	Gly	Gln	Gln	Thr	Ser	Trp	Lys	Ile	Ile	Ser	865	870	875
Tyr	Val	Leu	Thr	Pro	Gly	Ala	Thr	Ser	Ile	Ser	Asn	Leu	Asp	Leu	Lys	885	890	895
Ala	Ile	Phe	Ala	Asp	Ala	Ala	Ala	Arg	Gly	Ser	Leu	Asn	Thr	Ser	Asp	900	905	910
Tyr	Leu	Leu	Asp	Val	Glu	Ala	Gly	Phe	Glu	Ile	Trp	Gln	Gly	Gly	Gln	915	920	925
Gly	Leu	Gly	Ser	Asn	Ser	Phe	Ser	Val	Ser	Val	Thr	Ser	Gly	Gly	Val	930	935	940
Ala	Cys	Arg	Ala	Thr	Tyr	Val	Val	Asn	Ser	Asp	Trp	Gly	Ser	Gly	Phe	945	950	955
Thr	Ala	Thr	Val	Thr	Val	Thr	Asn	Thr	Gly	Ser	Arg	Ala	Thr	Asn	Gly	965	970	975
Trp	Thr	Val	Ala	Trp	Ser	Phe	Gly	Gly	Asn	Gln	Thr	Val	Thr	Asn	Tyr	980	985	990

Thr Ala Ser

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<210> 7
<211> 231
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Segment of  
GuxA

Thr Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala  
180 185 190

Ala Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala  
 195 200 205

Gly Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe  
 210 215 220

Ser Val Ser Val Thr Ser Gly  
 225 230

<210> 8  
 <211> 101  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Segment of  
 GuxA

<400> 8  
 Gly Val Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser  
 1 5 10 15  
 Gly Phe Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr  
 20 25 30  
 Asn Gly Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr  
 35 40 45  
 Asn Tyr Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala  
 50 55 60  
 Thr Asn Leu Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr  
 65 70 75 80  
 Phe Gly Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu  
 85 90 95  
 Ser Cys Thr Ala Ser  
 100

<210> 9  
 <211> 423  
 <212> PRT  
 <213> Acidothermus cellulolyticus

<400> 9  
 Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn  
 1 5 10 15  
 Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn  
 20 25 30  
 Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala  
 35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro  
 50 55 60  
 Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr  
 65 70 75 80  
 Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp  
 85 90 95  
 Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly  
 100 105 110  
 Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu  
 115 120 125  
 Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro  
 130 135 140  
 Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala  
 145 150 155 160  
 Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys  
 165 170 175  
 Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser  
 180 185 190  
 Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val  
 195 200 205  
 Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe  
 210 215 220  
 Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr  
 225 230 235 240  
 Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr  
 245 250 255  
 Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr  
 260 265 270  
 Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile  
 275 280 285  
 Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro  
 290 295 300  
 Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp  
 305 310 315 320  
 Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu  
 325 330 335  
 Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu  
 340 345 350

Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser  
 355 360 365

Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp  
 370 375 380

Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn  
 385 390 395 400

Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val  
 405 410 415

Ala Asn Ala Arg Pro Ala Val  
 420

<210> 10

<211> 430

<212> PRT

<213> Cellulomonas fimi

<400> 10

Ala Pro Val His Val Asp Asn Pro Tyr Ala Gly Ala Val Gln Tyr Val  
 1 5 10 15

Asn Pro Thr Trp Ala Ala Ser Val Asn Ala Ala Ala Gly Arg Gln Ser  
 20 25 30

Ala Asp Pro Ala Leu Ala Ala Lys Met Arg Thr Val Ala Gly Gln Pro  
 35 40 45

Thr Ala Val Trp Met Asp Arg Ile Ser Ala Ile Thr Gly Asn Ala Asp  
 50 55 60

Gly Asn Gly Leu Lys Phe His Leu Asp Asn Ala Val Ala Gln Gln Lys  
 65 70 75 80

Ala Ala Gly Val Pro Leu Val Phe Asn Leu Val Ile Tyr Asp Leu Pro  
 85 90 95

Gly Arg Asp Cys Phe Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr  
 100 105 110

Asp Ala Gly Leu Ala Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala  
 115 120 125

Asp Leu Leu Asp Asn Pro Glu Tyr Glu Ser Ile Arg Ile Ala Ala Thr  
 130 135 140

Ile Glu Pro Asp Ser Leu Pro Asn Leu Thr Thr Asn Ile Ser Glu Pro  
 145 150 155 160

Ala Cys Gln Gln Ala Ala Pro Tyr Tyr Arg Gln Gly Val Lys Tyr Ala  
 165 170 175

Leu Asp Lys Leu His Ala Ile Pro Asn Val Tyr Asn Tyr Ile Asp Ile  
 180 185 190



Gly His Ser Gly Trp Leu Gly Trp Asp Ser Asn Ala Gly Pro Ser Ala  
 195 200 205  
 Thr Leu Phe Ala Glu Val Ala Lys Ser Thr Thr Ala Gly Phe Ala Ser  
 210 215 220  
 Ile Asp Gly Phe Val Ser Asp Val Ala Asn Thr Thr Pro Leu Glu Glu  
 225 230 235 240  
 Pro Leu Leu Ser Asp Ser Ser Leu Thr Ile Asn Asn Thr Pro Ile Arg  
 245 250 255  
 Ser Ser Lys Phe Tyr Glu Trp Asn Phe Asp Phe Asp Glu Ile Asp Tyr  
 260 265 270  
 Thr Ala His Met His Arg Leu Leu Val Ala Ala Gly Phe Pro Ser Ser  
 275 280 285  
 Ile Gly Met Leu Val Asp Thr Ser Arg Asn Gly Trp Gly Gly Pro Asn  
 290 295 300  
 Arg Pro Thr Ser Ile Thr Ala Ser Thr Asp Val Asn Ala Tyr Val Asp  
 305 310 315 320  
 Ala Asn Arg Val Asp Arg Arg Val His Arg Gly Ala Trp Cys Asn Pro  
 325 330 335  
 Leu Gly Ala Gly Ile Gly Arg Phe Pro Glu Ala Thr Pro Ser Gly Tyr  
 340 345 350  
 Ala Ala Ser His Leu Asp Ala Phe Val Trp Ile Lys Pro Pro Gly Glu  
 355 360 365  
 Ser Asp Gly Ala Ser Thr Asp Ile Pro Asn Asp Gln Gly Lys Arg Phe  
 370 375 380  
 Asp Arg Met Cys Asp Pro Thr Phe Val Ser Pro Lys Leu Asn Asn Gln  
 385 390 395 400  
 Leu Thr Gly Ala Thr Pro Asn Ala Pro Leu Ala Gly Gln Trp Phe Glu  
 405 410 415  
 Glu Gln Phe Val Thr Leu Val Lys Asn Ala Tyr Pro Val Ile  
 420 425 430

<210> 11  
 <211> 432  
 <212> PRT  
 <213> Thermobifida fusca

<400> 11  
 Pro Gly Gly Pro Thr Asn Pro Pro Thr Asn Pro Gly Glu Lys Val Asp  
 1 5 10 15  
 Asn Pro Phe Glu Gly Ala Lys Leu Tyr Val Asn Pro Val Trp Ser Ala  
 20 25 30

Lys Ala Ala Ala Glu Pro Gly Gly Ser Ala Val Ala Asn Glu Ser Thr  
                   35                                  40                                  45  
 Ala Val Trp Leu Asp Arg Ile Gly Ala Ile Glu Gly Asn Asp Ser Pro  
           50                                  55                                  60  
 Thr Thr Gly Ser Met Gly Leu Arg Asp His Leu Glu Glu Ala Val Arg  
   65                                  70                                  75                                  80  
 Gln Ser Gly Gly Asp Pro Leu Thr Ile Gln Val Val Ile Tyr Asn Leu  
                                   85                                  90                                  95  
 Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Gly Pro  
                   100                                  105                                  110  
 Asp Glu Leu Asp Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala Asp  
           115                                  120                                  125  
 Ile Met Trp Asp Phe Ala Asp Tyr Glu Asn Leu Arg Ile Val Ala Ile  
   130                                  135                                  140  
 Ile Glu Ile Asp Ser Leu Pro Asn Leu Val Thr Asn Val Gly Gly Asn  
  145                                  150                                  155                                  160  
 Gly Gly Thr Glu Leu Cys Ala Tyr Met Lys Gln Asn Gly Gly Tyr Val  
                   165                                  170                                  175  
 Asn Gly Val Gly Tyr Ala Leu Arg Lys Leu Gly Glu Ile Pro Asn Val  
                   180                                  185                                  190  
 Tyr Asn Tyr Ile Asp Ala Ala His His Gly Trp Ile Gly Trp Asp Ser  
   195                                  200                                  205  
 Asn Phe Gly Pro Ser Val Asp Ile Phe Tyr Glu Ala Ala Asn Ala Ser  
   210                                  215                                  220  
 Gly Ser Thr Val Asp Tyr Val His Gly Phe Ile Ser Asn Thr Ala Asn  
  225                                  230                                  235                                  240  
 Tyr Ser Ala Thr Val Glu Pro Tyr Leu Asp Val Asn Gly Thr Val Asn  
                   245                                  250                                  255  
 Gly Gln Leu Ile Arg Gln Ser Lys Trp Val Asp Trp Asn Gln Tyr Val  
                   260                                  265                                  270  
 Asp Glu Leu Ser Phe Val Gln Asp Leu Arg Gln Ala Leu Ile Ala Lys  
   275                                  280                                  285  
 Gly Phe Arg Ser Asp Ile Gly Met Leu Ile Asp Thr Ser Arg Asn Gly  
   290                                  295                                  300  
 Trp Gly Gly Pro Asn Arg Pro Thr Gly Pro Ser Ser Ser Thr Asp Leu  
 • 305                                  310                                  315                                  320  
 Asn Thr Tyr Val Asp Glu Ser Arg Ile Asp Arg Arg Ile His Pro Gly  
                   325                                  330                                  335

Asn Trp Cys Asn Gln Ala Gly Ala Gly Leu Gly Glu Arg Pro Thr Val  
 340 345 350

Asn Pro Ala Pro Gly Val Asp Ala Tyr Val Trp Val Lys Pro Pro Gly  
 355 360 365

Glu Ser Asp Gly Ala Ser Glu Glu Ile Pro Asn Asp Glu Gly Lys Gly  
 370 375 380

Phe Asp Arg Met Cys Asp Pro Thr Tyr Gln Gly Asn Ala Arg Asn Gly  
 385 390 395 400

Asn Asn Pro Ser Gly Ala Leu Pro Asn Ala Pro Ile Ser Gly His Trp  
 405 410 415

Phe Ser Ala Gln Phe Arg Glu Leu Leu Ala Asn Ala Tyr Pro Pro Leu  
 420 425 430

<210> 12

<211> 221

<212> PRT

<213> Acidothermus cellulolyticus

<400> 12

Asn Gln Gln Ile Cys Asp Arg Tyr Gly Thr Thr Thr Ile Gln Asp Arg  
 1 5 10 15

Tyr Val Val Gln Asn Asn Arg Trp Gly Thr Ser Ala Thr Gln Cys Ile  
 20 25 30

Asn Val Thr Gly Asn Gly Phe Glu Ile Thr Gln Ala Asp Gly Ser Val  
 35 40 45

Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Tyr Asp Gly Cys  
 50 55 60

His Tyr Gly Asn Cys Ala Pro Arg Thr Thr Leu Pro Met Arg Ile Ser  
 65 70 75 80

Ser Ile Gly Ser Ala Pro Ser Ser Val Ser Tyr Arg Tyr Thr Gly Asn  
 85 90 95

Gly Val Tyr Asn Ala Ala Tyr Asp Ile Trp Leu Asp Pro Thr Pro Arg  
 100 105 110

Thr Asn Gly Val Asn Arg Thr Glu Ile Met Ile Trp Phe Asn Arg Val  
 115 120 125

Gly Pro Val Gln Pro Ile Gly Ser Pro Val Gly Thr Ala His Val Gly  
 130 135 140

Gly Arg Ser Trp Glu Val Trp Thr Gly Ser Asn Gly Ser Asn Asp Val  
 145 150 155 160

Trp Tyr Leu Thr Ser Val Gln Ala Gly Phe Glu Pro Trp Gln Asn Gly  
195 200 205

Ala Gly Leu Ala Val Asn Ser Phe Ser Ser Thr Val Glu  
 210 215 220

<210> 14

<211> 228

<212> PRT

<213> Streptomyces lividans

<400> 14

Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp  
 1 5 10 15

Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys  
 20 25 30

Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn  
 35 40 45

Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr  
 50 55 60

Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro  
 65 70 75 80

Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr  
 85 90 95

Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn  
 100 105 110

Ser Thr Pro Thr Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile  
 115 120 125

Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala  
 130 135 140

Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln  
 145 150 155 160

Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr  
 165 170 175

Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala  
 180 185 190

Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly  
 195 200 205

Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser  
 210 215 220

Val Ser Val Thr  
 225